This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rag.

start

```
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OM protein - protein search, using sw model

Run on:          April 26, 2006, 02:13:52 ; Search time 105.264 Seconds
                                             (without alignments)
                                             196.180 Million cell updates/sec

Title:           US-10-647-732A-2
Perfect score:   255
Sequence:        1 RSVRAQRHTDMPRTPKKPLS.........KEVHQKNSSRGNTGGRNYRM 47

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:       2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_21:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	255	100.0	47	3	AAY77405	Aay77405 Rainbow t
2	255	100.0	47	7	ADF56463	Adf56463 Rainbow t
3	244	95.7	47	7	ADD67520	Add67520 Rainbow t
4	244	95.7	47	8	ADP82542	Adp82542 Rainbow t
5	231.5	90.8	74	3	AAY77407	Aay77407 Rainbow t
6	231.5	90.8	74	7	ADF56465	Adf56465 Rainbow t
7	220.5	86.5	74	7	ADD67518	Add67518 Rainbow t

8	220.5	86.5	74	8	ADP82540	Adp82540	Rainbow t
9	198.5	77.8	186	2	AAR72472	Aar72472	Flatfish
10	198.5	77.8	186	8	ADV95289	Adv95289	Rockfish
11	172	67.5	35	3	AAY77404	Aay77404	Rainbow t
12	172	67.5	35	7	ADD67521	Add67521	Rainbow t
13	172	67.5	35	7	ADF56462	Adf56462	Rainbow t
14	172	67.5	35	8	ADP82543	Adp82543	Rainbow t
15	168.5	66.1	62	3	AAY77406	Aay77406	Rainbow t
16	168.5	66.1	62	7	ADD67519	Add67519	Rainbow t
17	168.5	66.1	62	7	ADF56464	Adf56464	Rainbow t
18	168.5	66.1	62	8	ADP82541	Adp82541	Rainbow t
19	168.5	66.1	176	2	AAR88089	Aar88089	Rainbow t
20	132	51.8	105	4	AAE02452	Aae02452	Rabbit li
21	132	51.8	105	4	AAE02450	Aae02450	Human liv
22	132	51.8	105	4	AAE02456	Aae02456	Rabbit li
23	132	51.8	105	5	AAU10562	Aau10562	Human ins
24	132	51.8	105	5	AAU10564	Aau10564	Rabbit in
25	132	51.8	105	7	ABR63172	Abr63172	Rabbit li
26	132	51.8	105	7	ABR63170	Abr63170	Human liv
27	132	51.8	105	9	ADZ58808	Adz58808	Human mat
28	132	51.8	119	1	AAP60578	Aap60578	Human pre
29	132	51.8	130	9	AEB70451	Aeb70451	Insulin-1
30	132	51.8	137	4	AAU09067	Aau09067	Human ins
31	132	51.8	137	8	ADU46866	Adu46866	Insulin-1
32	132	51.8	137	9	AEB70455	Aeb70455	Insulin-1
33	132	51.8	137	9	AEB70450	Aeb70450	Insulin-1
34	132	51.8	153	2	AAR83803	Aar83803	Insulin-1
35	132	51.8	153	2	AAW69733	Aaw69733	Human IGF
36	132	51.8	153	2	AAW57882	Aaw57882	Human IGF
37	132	51.8	153	5	AAU84284	Aau84284	Human end
38	132	51.8	153	5	AAU84341	Aau84341	Protein I
39	132	51.8	153	6	ADA26451	Ada26451	Human ins
40	132	51.8	153	7	ADC59343	Adc59343	Human ins
41	132	51.8	153	7	ADD25494	Add25494	Binding d
42	132	51.8	153	7	ADP65213	Adp65213	Human ins
43	132	51.8	153	8	ADH10374	Adh10374	Human ins
44	132	51.8	153	8	ABO84602	Abo84602	Human can
45	132	51.8	153	8	ADS73976	Ads73976	Insulin-1

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rai.

<u>start</u>

<u>Go Back to previous page</u>

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OM protein - protein search, using sw model

Run on:          April 26, 2006, 02:23:52 ; Search time 26.0248 Seconds
                                            (without alignments)
                                            149.310 Million cell updates/sec


Title:           US-10-647-732A-2
Perfect score:   255
Sequence:        1 RSVRAQRHTDMPRTPKKPLS.........KEVHQKNSSRGNTGGRNYRM 47

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:        572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
                 1:  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2:  /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                              SUMMARIES
                    %
Result            Query
   No.   Score    Match Length DB   ID                     Description
-----------------------------------------------------------------------------
     1     255    100.0    47   2   US-09-120-818-2        Sequence 2, Appli
     2     255    100.0    47   2   US-09-609-642-2        Sequence 2, Appli
     3     255    100.0    47   2   US-09-669-642-2        Sequence 2, Appli
     4   231.5     90.8    74   2   US-09-120-818-4        Sequence 4, Appli
     5   231.5     90.8    74   2   US-09-609-642-4        Sequence 4, Appli
     6   231.5     90.8    74   2   US-09-669-642-4        Sequence 4, Appli
     7     172     67.5    35   2   US-09-120-818-1        Sequence 1, Appli
     8     172     67.5    35   2   US-09-609-642-1        Sequence 1, Appli
     9     172     67.5    35   2   US-09-669-642-1        Sequence 1, Appli
    10   168.5     66.1    62   2   US-09-120-818-3        Sequence 3, Appli
```

11	168.5	66.1	62	2	US-09-609-642-3	Sequence 3, Appli
12	168.5	66.1	62	2	US-09-669-642-3	Sequence 3, Appli
13	168.5	66.1	176	1	US-07-953-230A-9	Sequence 9, Appli
14	132	51.8	105	2	US-09-852-261-10	Sequence 10, Appl
15	132	51.8	105	2	US-09-852-261-14	Sequence 14, Appl
16	132	51.8	119	6	5405942-1	Patent No. 5405942
17	132	51.8	127	2	US-09-617-389B-18	Sequence 18, Appl
18	132	51.8	137	1	US-07-953-230A-10	Sequence 10, Appl
19	132	51.8	152	2	US-08-950-720A-9	Sequence 9, Appli
20	132	51.8	153	1	US-08-219-878A-1	Sequence 1, Appli
21	132	51.8	153	2	US-09-917-254-82	Sequence 82, Appl
22	132	51.8	153	2	US-09-919-497-74	Sequence 74, Appl
23	132	51.8	153	4	PCT-US93-04329-1	Sequence 1, Appli
24	132	51.8	156	2	US-09-142-583A-11	Sequence 11, Appl
25	132	51.8	184	2	US-09-949-016-7523	Sequence 7523, Ap
26	132	51.8	191	2	US-08-989-251-41	Sequence 41, Appl
27	132	51.8	191	2	US-09-340-250-41	Sequence 41, Appl
28	132	51.8	191	2	US-09-528-108-41	Sequence 41, Appl
29	132	51.8	191	2	US-09-921-398-41	Sequence 41, Appl
30	132	51.8	191	2	US-10-280-826-41	Sequence 41, Appl
31	125	49.0	105	2	US-09-852-261-12	Sequence 12, Appl
32	85.5	33.5	110	2	US-09-852-261-2	Sequence 2, Appli
33	83	32.5	111	2	US-09-852-261-6	Sequence 6, Appli
34	83	32.5	121	2	US-09-142-583A-4	Sequence 4, Appli
35	79.5	31.2	111	2	US-09-852-261-4	Sequence 4, Appli
36	74	29.0	19	2	US-09-142-583A-6	Sequence 6, Appli
37	61.5	24.1	204	2	US-09-134-001C-4814	Sequence 4814, Ap
38	59	23.1	508	1	US-08-818-024-3	Sequence 3, Appli
39	59	23.1	508	2	US-09-334-775A-3	Sequence 3, Appli
40	58.5	22.9	388	2	US-09-270-767-58024	Sequence 58024, A
41	58.5	22.9	1113	2	US-09-270-767-42704	Sequence 42704, A
42	57.5	22.5	407	2	US-09-538-092-656	Sequence 656, App
43	57	22.4	588	1	US-08-391-615-5	Sequence 5, Appli
44	56.5	22.2	191	2	US-09-489-039A-13754	Sequence 13754, A
45	56.5	22.2	1064	2	US-09-926-820-1	Sequence 1, Appli

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rapbm.

start

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OM protein - protein search, using sw model

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Run on:            April 26, 2006, 02:24:43 ; Search time 92.4463 Seconds
                                             (without alignments)
                                             212.426 Million cell updates/sec
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```
Title:             US-10-647-732A-2
Perfect score:     255
Sequence:          1 RSVRAQRHTDMPRTPKKPLS.........KEVHQKNSSRGNTGGRNYRM 47
```

```
Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5
```

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Searched:          1867569 seqs, 417829326 residues
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Total number of hits satisfying chosen parameters: 1867569

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

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Database :         Published_Applications_AA_Main:*
                   1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                   2:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                   3:  /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                   4:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                   5:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                   6:  /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
```

```
        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

```
                                SUMMARIES
                    %
Result            Query
   No.    Score  Match Length DB   ID                       Description
-------------------------------------------------------------------------------
     1      244   95.7     47  4   US-10-100-492-4          Sequence 4, Appli
     2    220.5   86.5     74  4   US-10-100-492-2          Sequence 2, Appli
     3    198.5   77.8    186  6   US-11-049-518-27         Sequence 27, Appl
     4      172   67.5     35  4   US-10-100-492-5          Sequence 5, Appli
     5    168.5   66.1     62  4   US-10-100-492-3          Sequence 3, Appli
     6      132   51.8    105  3   US-09-852-261-10         Sequence 10, Appl
     7      132   51.8    105  3   US-09-852-261-14         Sequence 14, Appl
     8      132   51.8    105  5   US-10-504-078-10         Sequence 10, Appl
     9      132   51.8    105  5   US-10-504-078-14         Sequence 14, Appl
    10      132   51.8    105  5   US-10-688-821-53         Sequence 53, Appl
```

11	132	51.8	127	4	US-10-700-725-18	Sequence 18, Appl
12	132	51.8	130	6	US-11-049-518-25	Sequence 25, Appl
13	132	51.8	137	4	US-10-251-661-8	Sequence 8, Appli
14	132	51.8	153	3	US-09-919-497-74	Sequence 74, Appl
15	132	51.8	153	3	US-09-861-101-5	Sequence 5, Appli
16	132	51.8	153	4	US-10-136-639-3	Sequence 3, Appli
17	132	51.8	153	4	US-10-207-655-55	Sequence 55, Appl
18	132	51.8	153	4	US-10-460-550-5	Sequence 5, Appli
19	132	51.8	153	4	US-10-706-791-2	Sequence 2, Appli
20	132	51.8	153	5	US-10-851-921-2	Sequence 2, Appli
21	132	51.8	153	5	US-10-461-862-68	Sequence 68, Appl
22	132	51.8	153	5	US-10-460-550-5	Sequence 5, Appli
23	132	51.8	153	5	US-10-287-436A-455	Sequence 455, App
24	132	51.8	153	5	US-10-287-436A-1154	Sequence 1154, Ap
25	132	51.8	153	5	US-10-798-896-4	Sequence 4, Appli
26	132	51.8	191	3	US-09-921-398-41	Sequence 41, Appl
27	132	51.8	191	3	US-09-967-768-41	Sequence 41, Appl
28	132	51.8	191	4	US-10-280-826-41	Sequence 41, Appl
29	132	51.8	191	6	US-11-046-099-41	Sequence 41, Appl
30	127	49.8	105	4	US-10-238-114-3	Sequence 3, Appli
31	127	49.8	153	4	US-10-238-114-2	Sequence 2, Appli
32	125	49.0	105	3	US-09-852-261-12	Sequence 12, Appl
33	125	49.0	105	5	US-10-504-078-12	Sequence 12, Appl
34	88.5	34.7	77	4	US-10-100-492-1	Sequence 1, Appli
35	88.5	34.7	195	4	US-10-443-466A-20	Sequence 20, Appl
36	88.5	34.7	195	4	US-10-706-791-3	Sequence 3, Appli
37	88.5	34.7	195	5	US-10-461-862-66	Sequence 66, Appl
38	86	33.7	133	4	US-10-161-088-2	Sequence 2, Appli
39	86	33.7	133	5	US-10-461-862-63	Sequence 63, Appl
40	85.5	33.5	110	3	US-09-852-261-2	Sequence 2, Appli
41	85.5	33.5	110	5	US-10-504-078-2	Sequence 2, Appli
42	83	32.5	111	3	US-09-852-261-6	Sequence 6, Appli
43	83	32.5	111	5	US-10-504-078-6	Sequence 6, Appli
44	80	31.4	104	6	US-11-049-518-17	Sequence 17, Appl
45	79.5	31.2	111	3	US-09-852-261-4	Sequence 4, Appli

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rapbn.
start

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:25:58 ; Search time 13.2066 Seconds
                                          (without alignments)
                                          156.599 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS..........KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
----
    1   255 100.0   47 6   US-10-647-732A-2   Sequence 2, Appli
    2   231.5   90.8   74 6   US-10-647-732A-4   Sequence 4, Appli
    3   172   67.5   35 6   US-10-647-732A-1   Sequence 1, Appli
    4   168.5   66.1   62 6   US-10-647-732A-3   Sequence 3, Appli
    5   132   51.8   105 7   US-11-228-458-10   Sequence 10, Appl
    6   132   51.8   105 7   US-11-228-458-14   Sequence 14, Appl
    7   132   51.8   130 7   US-11-043-788-222   Sequence 222, App
    8   132   51.8   137 7   US-11-043-788-221   Sequence 221, App

9	132	51.8	137	7	US-11-043-788-226	Sequence 226, App
10	132	51.8	153	7	US-11-043-788-223	Sequence 223, App
11	132	51.8	153	7	US-11-043-788-228	Sequence 228, App
12	132	51.8	153	7	US-11-244-925-4	Sequence 4, Appli
13	132	51.8	567	6	US-10-954-468-8	Sequence 8, Appli
14	132	51.8	574	6	US-10-954-468-4	Sequence 4, Appli
15	132	51.8	580	6	US-10-954-468-6	Sequence 6, Appli
16	132	51.8	587	6	US-10-954-468-2	Sequence 2, Appli
17	132	51.8	615	6	US-10-954-468-7	Sequence 7, Appli
18	132	51.8	622	6	US-10-954-468-3	Sequence 3, Appli
19	132	51.8	628	6	US-10-954-468-5	Sequence 5, Appli
20	132	51.8	633	6	US-10-954-468-1	Sequence 1, Appli
21	125	49.0	105	7	US-11-228-458-12	Sequence 12, Appl
22	88.5	34.7	195	7	US-11-043-788-220	Sequence 220, App
23	88.5	34.7	195	7	US-11-043-788-227	Sequence 227, App
24	85.5	33.5	110	7	US-11-228-458-2	Sequence 2, Appli
25	85.5	33.5	139	7	US-11-043-788-224	Sequence 224, App
26	85.5	33.5	142	7	US-11-043-788-225	Sequence 225, App
27	83	32.5	111	7	US-11-228-458-6	Sequence 6, Appli
28	79.5	31.2	111	7	US-11-228-458-4	Sequence 4, Appli
29	74	29.0	19	7	US-11-043-788-487	Sequence 487, App
30	55.5	21.8	121	6	US-10-678-790-63	Sequence 63, Appl
31	55.5	21.8	238	7	US-11-194-890-12	Sequence 12, Appl
32	55.5	21.8	267	7	US-11-194-890-11	Sequence 11, Appl
33	54	21.2	948	6	US-10-523-477-14	Sequence 14, Appl
34	54	21.2	964	7	US-11-024-959-477	Sequence 477, App
35	53	20.8	643	7	US-11-137-465-54	Sequence 54, Appl
36	53	20.8	653	7	US-11-137-465-55	Sequence 55, Appl
37	52.5	20.6	373	7	US-11-188-298-370	Sequence 370, App
38	52.5	20.6	1112	7	US-11-188-298-16876	Sequence 16876, A
39	52	20.4	438	7	US-11-024-959-342	Sequence 342, App
40	52	20.4	663	7	US-11-087-099-7915	Sequence 7915, Ap
41	52	20.4	723	7	US-11-072-512-2246	Sequence 2246, Ap
42	52	20.4	2444	7	US-11-188-298-17072	Sequence 17072, A
43	51.5	20.2	107	6	US-10-678-790-61	Sequence 61, Appl
44	51.5	20.2	122	6	US-10-678-790-60	Sequence 60, Appl
45	51.5	20.2	507	6	US-10-330-773-187	Sequence 187, App

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rpr.

<u>start</u>

<u>Go Back to previous page</u>

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:19:02 ; Search time 19.0331 Seconds
                                           (without alignments)
                                           237.596 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.........KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	255	100.0	161	2	C54270	insulin-like growt
2	231.5	90.8	188	2	A54270	insulin-like growt
3	231.5	90.8	188	2	B54270	insulin-like growt
4	191.5	75.1	155	2	C44012	insulin-like growt
5	172	67.5	149	2	D54270	insulin-like growt
6	168.5	66.1	176	2	A41396	insulin-like growt
7	168.5	66.1	176	2	A46244	insulin-like growt
8	140	54.9	153	2	A41399	insulin-like growt
9	132	51.8	137	1	IGGP1	insulin-like growt
10	132	51.8	137	2	A36552	insulin-like growt
11	132	51.8	153	1	IGHU1	insulin-like growt
12	131	51.4	153	2	A36079	insulin-like growt

13	128	50.2	153	2	S12825	insulin-like growt
14	127	49.8	138	2	S22878	insulin-like growt
15	127	49.8	153	1	IGBO1	insulin-like growt
16	127	49.8	154	2	JC2483	insulin-like growt
17	127	49.8	154	2	A33390	insulin-like growt
18	125	49.0	127	2	B40912	insulin-like growt
19	125	49.0	127	2	A25540	insulin-like growt
20	.125	49.0	153	2	B27804	insulin-like growt
21	111	43.5	122	2	PN0622	insulin-like growt
22	96	37.6	193	2	A53697	insulin-like growt
23	90	35.3	181	2	A27804	insulin-like growt
24	88.5	34.7	195	1	IGHU1B	insulin-like growt
25	79.5	31.2	133	2	A40912	insulin-like growt
26	79.5	31.2	159	2	A26859	insulin-like growt
27	69.5	27.3	79	2	I51240	insulin-like growt
28	60.5	23.7	145	2	A87574	hypothetical prote
29	59	23.1	263	2	S64472	hypothetical prote
30	59	23.1	508	2	T22440	hypothetical prote
31	59	23.1	817	2	T22442	hypothetical prote
32	58	22.7	1106	2	JQ0405	hypothetical 119.5
33	58	22.7	1186	2	T19050	hypothetical prote
34	57.5	22.5	407	2	S53900	hypothetical prote
35	57.5	22.5	509	2	T31797	hypothetical prote
36	57	22.4	590	1	TVFFDS	protein-tyrosine k
37	57	22.4	751	1	TVVPTH	large T antigen -
38	56.5	22.2	1206	2	E86445	hypothetical prote
39	56	22.0	433	2	T46512	probable serine/th
40	56	22.0	816	2	T27189	hypothetical prote
41	55.5	21.8	321	2	S62015	SOL1 protein - yea
42	55.5	21.8	511	2	S58399	cellutagmin I sytV
43	55.5	21.8	564	2	A38271	serotonin receptor
44	55	21.6	55	1	VHNVAC	nucleocapsid prote
45	55	21.6	151	2	T43960	hypothetical prote

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rup.

start

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:14:17 ; Search time 113.421 Seconds
                                             (without alignments)
                                             292.359 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.........KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   255   100.0   161   2   Q91230_ONCTS   Q91230 oncorhynchu
    2   237   92.9   161   2   Q90VV9_BRARE   Q90vv9 brachydanio
    3   235   92.2   161   1   IGF1A_CYPCA   Q90325 cyprinus ca
    4   234   91.8   159   2   Q6V293_ICTPU   Q6v293 ictalurus p
    5   231.5   90.8   188   1   IGF1_ONCKI   P17085 oncorhynchu
    6   231.5   90.8   188   2   Q91965_ONCTS   Q91965 oncorhynchu
    7   225   88.2   161   2   Q506L8_9TELE   Q50618 cirrhinus m
    8   217   85.1   117   2   Q9I9I4_CTEID   Q9i9i4 ctenopharyn
    9   217   85.1   161   2   Q800D5_9TELE   Q800d5 megalobrama
   10   217   85.1   161   2   Q98SR6_MEGAM   Q98sr6 megalobrama
   11   216   84.7   159   2   O93607_PAROL   O93607 paralichthy
   12   216   84.7   178   2   Q5BQH3_9TELE   Q5bqh3 gymnocypris
   13   214.5   84.1   160   2   Q70BT5_PERFL   Q70bt5 perca fluvi
   14   212   83.1   161   2   Q9PWK2_CARAU   Q9pwk2 carassius a

15	212	83.1	161	2	Q9YI82_CARAU	Q9yi82	carassius a
16	211	82.7	161	1	IGF1B_CYPCA	Q90326	cyprinus ca
17	211	82.7	178	2	Q9IBI0_CYPCA	Q9ibi0	cyprinus ca
18	208.5	81.8	186	2	Q800Y5_SIGGU	Q800y5	siganus gut
19	198.5	77.8	186	2	Q5Q0U4_DICLA	Q5q0u4	dicentrarch
20	198.5	77.8	186	2	Q5U8T6_EPICO	Q5u8t6	epinephelus
21	198.5	77.8	186	2·	Q6R527_EPICO	Q6r527	epinephelus
22	198.5	77.8	186	2	Q6T8S2_MUGCE	Q6t8s2	mugil cepha
23	198.5	77.8	186	2	Q70BT6_PERFL	Q70bt6	perca fluvi
24	198.5	77.8	186	2	Q7T1A7_PERFV	Q7t1a7	perca flave
25	198.5	77.8	186	2	Q9PSX5_PAROL	Q9psx5	paralichthy
26	194.5	76.3	186	2	O93527_PAROL	O93527	paralichthy
27	187.5	73.5	185	2	Q9YI57_ACASC	Q9yi57	acanthopagr
28	187.5	73.5	185	2	Q4G1F3_SPAAU	Q4g1f3	sparus aura
29	172	67.5	149	2	Q91231_ONCTS	Q91231	oncorhynchu
30	168.5	66.1	176	1	IGF1_ONCMY	Q02815	oncorhynchu
31	163.5	64.1	182	2	O42289_OREMO	O42289	oreochromis
32	163.5	64.1	182	2	O73720_OREMO	O73720	oreochromis
33	163.5	64.1	182	2	P79824_OREMO	P79824	oreochromis
34	160.5	62.9	184	2	O42336_MYOSC	O42336	myoxocephal
35	140	54.9	124	1	IGF1_COTJA	P51462	coturnix co
36	140	54.9	153	1	IGF1_CHICK	P18254	gallus gall
37	137	53.7	153	2	O93380_MELGA	O93380	meleagris g
38	132	51.8	130	1	IGF1_CAVPO	P17647	cavia porce
39	132	51.8	130	2	Q9NP10_HUMAN	Q9np10	homo sapien
40	132	51.8	137	2	Q14620_HUMAN	Q14620	homo sapien
41	132	51.8	153	1	IGF1A_HUMAN	P01343	homo sapien
42	132	51.8	153	2	Q5U743_HUMAN	Q5u743	homo sapien
43	132	51.8	184	2	Q59GC5_HUMAN	Q59gc5	homo sapien
44	131	51.4	153	1	IGF1_XENLA	P16501	xenopus lae
45	128	50.2	153	1	IGF1_PIG	P16545	sus scrofa

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rag.

<u>start</u>

<u>Go Back to previous page</u>

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OM protein - protein search, using sw model

Run on:            April 26, 2006, 02:13:52 ; Search time 165.736 Seconds
                                              (without alignments)
                                              196.180 Million cell updates/sec

Title:            US-10-647-732A-4
Perfect score:    393
Sequence:         1 RSVRAQRHTDMPRTPKVSTA..........KEVHQKNSSRGNTGGRNYRM 74

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:       2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        A_Geneseq_21:*
                  1:  geneseqp1980s:*
                  2:  geneseqp1990s:*
                  3:  geneseqp2000s:*
                  4:  geneseqp2001s:*
                  5:  geneseqp2002s:*
                  6:  geneseqp2003as:*
                  7:  geneseqp2003bs:*
                  8:  geneseqp2004s:*
                  9:  geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	74	3	AAY77407	Aay77407 Rainbow t
2	393	100.0	74	7	ADF56465	Adf56465 Rainbow t
3	382	97.2	74	7	ADD67518	Add67518 Rainbow t
4	382	97.2	74	8	ADP82540	Adp82540 Rainbow t
5	326	83.0	186	2	AAR72472	Aar72472 Flatfish
6	326	83.0	186	8	ADV95289	Adv95289 Rockfish
7	299	76.1	62	3	AAY77406	Aay77406 Rainbow t

8	299	76.1	62	7	ADD67519	Add67519 Rainbow t
9	299	76.1	62	7	ADF56464	Adf56464 Rainbow t
10	299	76.1	62	8	ADP82541	Adp82541 Rainbow t
11	299	76.1	176	2	AAR88089	Aar88089 Rainbow t
12	231.5	58.9	47	3	AAY77405	Aay77405 Rainbow t
13	231.5	58.9	47	7	ADF56463	Adf56463 Rainbow t
14	220.5	56.1	47	7	ADD67520	Add67520 Rainbow t
15	220.5	56.1	47	8	ADP82542	Adp82542 Rainbow t
16	220	56.0	185	3	ABB06295	Abb06295 Paralicht
17	160	40.7	178	9	AEB07519	Aeb07519 Korean ro
18	158.5	40.3	35	3	AAY77404	Aay77404 Rainbow t
19	158.5	40.3	35	7	ADD67521	Add67521 Rainbow t
20	158.5	40.3	35	7	ADF56462	Adf56462 Rainbow t
21	158.5	40.3	35	8	ADP82543	Adp82543 Rainbow t
22	118.5	30.2	105	4	AAE02452	Aae02452 Rabbit li
23	118.5	30.2	105	4	AAE02450	Aae02450 Human liv
24	118.5	30.2	105	4	AAE02456	Aae02456 Rabbit li
25	118.5	30.2	105	5	AAU10562	Aau10562 Human ins
26	118.5	30.2	105	5	AAU10564	Aau10564 Rabbit in
27	118.5	30.2	105	7	ABR63172	Abr63172 Rabbit li
28	118.5	30.2	105	7	ABR63170	Abr63170 Human liv
29	118.5	30.2	105	9	ADZ58808	Adz58808 Human mat
30	118.5	30.2	119	1	AAP60578	Aap60578 Human pre
31	118.5	30.2	130	9	AEB70451	Aeb70451 Insulin-l
32	118.5	30.2	137	4	AAU09067	Aau09067 Human ins
33	118.5	30.2	137	8	ADU46866	Adu46866 Insulin-l
34	118.5	30.2	137	9	AEB70455	Aeb70455 Insulin-l
35	118.5	30.2	137	9	AEB70450	Aeb70450 Insulin-l
36	118.5	30.2	153	2	AAR83803	Aar83803 Insulin-l
37	118.5	30.2	153	2	AAW69733	Aaw69733 Human IGF
38	118.5	30.2	153	2	AAW57882	Aaw57882 Human IGF
39	118.5	30.2	153	5	AAU84284	Aau84284 Human end
40	118.5	30.2	153	5	AAU84341	Aau84341 Protein I
41	118.5	30.2	153	6	ADA26451	Ada26451 Human ins
42	118.5	30.2	153	7	ADC59343	Adc59343 Human ins
43	118.5	30.2	153	7	ADD25494	Add25494 Binding d
44	118.5	30.2	153	7	ADP65213	Adp65213 Human ins
45	118.5	30.2	153	8	ADH10374	Adh10374 Human ins

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rai.

start

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:23:52 ; Search time 40.9752 Seconds
                                           (without alignments)
                                           149.310 Million cell updates/sec

Title: US-10-647-732A-4
Perfect score: 393
Sequence: 1 RSVRAQRHTDMPRTPKVSTA.........KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	74	2	US-09-120-818-4	Sequence 4, Appli
2	393	100.0	74	2	US-09-609-642-4	Sequence 4, Appli
3	393	100.0	74	2	US-09-669-642-4	Sequence 4, Appli
4	299	76.1	62	2	US-09-120-818-3	Sequence 3, Appli
5	299	76.1	62	2	US-09-609-642-3	Sequence 3, Appli
6	299	76.1	62	2	US-09-669-642-3	Sequence 3, Appli
7	299	76.1	176	1	US-07-953-230A-9	Sequence 9, Appli
8	231.5	58.9	47	2	US-09-120-818-2	Sequence 2, Appli
9	231.5	58.9	47	2	US-09-609-642-2	Sequence 2, Appli
10	231.5	58.9	47	2	US-09-669-642-2	Sequence 2, Appli

11	158.5	40.3	35	2	US-09-120-818-1	Sequence 1, Appli
12	158.5	40.3	35	2	US-09-609-642-1	Sequence 1, Appli
13	158.5	40.3	35	2	US-09-669-642-1	Sequence 1, Appli
14	118.5	30.2	105	2	US-09-852-261-10	Sequence 10, Appl
15	118.5	30.2	105	2	US-09-852-261-14	Sequence 14, Appl
16	118.5	30.2	119	6	5405942-1	Patent No. 5405942
17	118.5	30.2	127	2	US-09-617-389B-18	Sequence 18, Appl
18	118.5	30.2	137	1	US-07-953-230A-10	Sequence 10, Appl
19	118.5	30.2	152	2	US-08-950-720A-9	Sequence 9, Appli
20	118.5	30.2	153	1	US-08-219-878A-1	Sequence 1, Appli
21	118.5	30.2	153	2	US-09-917-254-82	Sequence 82, Appl
22	118.5	30.2	153	2	US-09-919-497-74	Sequence 74, Appl
23	118.5	30.2	153	4	PCT-US93-04329-1	Sequence 1, Appli
24	118.5	30.2	156	2	US-09-142-583A-11	Sequence 11, Appl
25	118.5	30.2	184	2	US-09-949-016-7523	Sequence 7523, Ap
26	118.5	30.2	191	2	US-08-989-251-41	Sequence 41, Appl
27	118.5	30.2	191	2	US-09-340-250-41	Sequence 41, Appl
28	118.5	30.2	191	2	US-09-528-108-41	Sequence 41, Appl
29	118.5	30.2	191	2	US-09-921-398-41	Sequence 41, Appl
30	118.5	30.2	191	2	US-10-280-826-41	Sequence 41, Appl
31	111.5	28.4	105	2	US-09-852-261-12	Sequence 12, Appl
32	83	21.1	110	2	US-09-852-261-2	Sequence 2, Appli
33	81	20.6	111	2	US-09-852-261-6	Sequence 6, Appli
34	81	20.6	121	2	US-09-142-583A-4	Sequence 4, Appli
35	79.5	20.2	454	2	US-09-080-044-4	Sequence 4, Appli
36	79.5	20.2	454	2	US-09-531-857A-4	Sequence 4, Appli
37	78	19.8	111	2	US-09-852-261-4	Sequence 4, Appli
38	74	18.8	19	2	US-09-142-583A-6	Sequence 6, Appli
39	68.5	17.4	312	2	US-09-252-991A-17496	Sequence 17496, A
40	65	16.5	212	2	US-09-252-991A-19925	Sequence 19925, A
41	64.5	16.4	186	2	US-09-252-991A-27476	Sequence 27476, A
42	64.5	16.4	216	2	US-09-252-991A-32065	Sequence 32065, A
43	64.5	16.4	389	2	US-09-949-016-6442	Sequence 6442, Ap
44	64.5	16.4	417	2	US-09-949-016-10594	Sequence 10594, A
45	63.5	16.2	429	2	US-09-252-991A-29079	Sequence 29079, A

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rapbm.
 start

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OM protein - protein search, using sw model

Run on:           April 26, 2006, 02:24:43 ; Search time 145.554 Seconds
                                            (without alignments)
                                            212.426 Million cell updates/sec

Title:            US-10-647-732A-4
Perfect score:    393
Sequence:         1 RSVRAQRHTDMPRTPKVSTA.........KEVHQKNSSRGNTGGRNYRM 74

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:       1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_Main:*
                  1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                  2:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                  3:  /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                  4:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  5:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  6:  /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result            Query
   No.   Score  Match  Length DB  ID                      Description
-----------------------------------------------------------------------------
     1    382    97.2     74   4  US-10-100-492-2         Sequence 2, Appli
     2    326    83.0    186   6  US-11-049-518-27        Sequence 27, Appl
     3    299    76.1     62   4  US-10-100-492-3         Sequence 3, Appli
     4  220.5    56.1     47   4  US-10-100-492-4         Sequence 4, Appli
     5  158.5    40.3     35   4  US-10-100-492-5         Sequence 5, Appli
     6  118.5    30.2    105   3  US-09-852-261-10        Sequence 10, Appl
     7  118.5    30.2    105   3  US-09-852-261-14        Sequence 14, Appl
     8  118.5    30.2    105   5  US-10-504-078-10        Sequence 10, Appl
     9  118.5    30.2    105   5  US-10-504-078-14        Sequence 14, Appl
    10  118.5    30.2    105   5  US-10-688-821-53        Sequence 53, Appl
```

11	118.5	30.2	127	4	US-10-700-725-18	Sequence 18, Appl
12	118.5	30.2	130	6	US-11-049-518-25	Sequence 25, Appl
13	118.5	30.2	137	4	US-10-251-661-8	Sequence 8, Appli
14	118.5	30.2	153	3	US-09-919-497-74	Sequence 74, Appl
15	118.5	30.2	153	3	US-09-861-101-5	Sequence 5, Appli
16	118.5	30.2	153	4	US-10-136-639-3	Sequence 3, Appli
17	118.5	30.2	153	4	US-10-207-655-55	Sequence 55, Appl
18	118.5	30.2	153	4	US-10-460-550-5	Sequence 5, Appli
19	118.5	30.2	153	4	US-10-706-791-2	Sequence 2, Appli
20	118.5	30.2	153	5	US-10-851-921-2	Sequence 2, Appli
21	118.5	30.2	153	5	US-10-461-862-68	Sequence 68, Appl
22	118.5	30.2	153	5	US-10-460-550-5	Sequence 5, Appli
23	118.5	30.2	153	5	US-10-287-436A-455	Sequence 455, App
24	118.5	30.2	153	5	US-10-287-436A-1154	Sequence 1154, Ap
25	118.5	30.2	153	5	US-10-798-896-4	Sequence 4, Appli
26	118.5	30.2	191	3	US-09-921-398-41	Sequence 41, Appl
27	118.5	30.2	191	3	US-09-967-768-41	Sequence 41, Appl
28	118.5	30.2	191	4	US-10-280-826-41	Sequence 41, Appl
29	118.5	30.2	191	6	US-11-046-099-41	Sequence 41, Appl
30	113.5	28.9	105	4	US-10-238-114-3	Sequence 3, Appli
31	113.5	28.9	153	4	US-10-238-114-2	Sequence 2, Appli
32	111.5	28.4	105	3	US-09-852-261-12	Sequence 12, Appl
33	111.5	28.4	105	5	US-10-504-078-12	Sequence 12, Appl
34	93	23.7	77	4	US-10-100-492-1	Sequence 1, Appli
35	93	23.7	195	4	US-10-443-466A-20	Sequence 20, Appl
36	93	23.7	195	4	US-10-706-791-3	Sequence 3, Appli
37	93	23.7	195	5	US-10-461-862-66	Sequence 66, Appl
38	83	21.1	110	3	US-09-852-261-2	Sequence 2, Appli
39	83	21.1	110	5	US-10-504-078-2	Sequence 2, Appli
40	81	20.6	111	3	US-09-852-261-6	Sequence 6, Appli
41	81	20.6	111	5	US-10-504-078-6	Sequence 6, Appli
42	80	20.4	104	6	US-11-049-518-17	Sequence 17, Appl
43	78	19.8	111	3	US-09-852-261-4	Sequence 4, Appli
44	78	19.8	111	5	US-10-504-078-4	Sequence 4, Appli
45	78	19.8	133	4	US-10-161-088-2	Sequence 2, Appli

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rapbn.

start

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OM protein - protein search, using sw model

Run on:              April 26, 2006, 02:25:58 ; Search time 20.7934 Seconds
                                                (without alignments)
                                                156.599 Million cell updates/sec

Title:               US-10-647-732A-4
Perfect score:       393
Sequence:            1 RSVRAQRHTDMPRTPKVSTA..........KEVHQKNSSRGNTGGRNYRM 74

Scoring table:       BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched:            225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters:        225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :           Published_Applications_AA_New:*
                     1:  /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                     2:  /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                     3:  /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                     4:  /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                     5:  /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                     6:  /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                     7:  /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                     8:  /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
```

```
            %
Result      Query
No.    Score Match Length DB  ID                      Description
-----------------------------------------------------------------------------
     1   393 100.0    74  6   US-10-647-732A-4        Sequence 4, Appli
     2   299  76.1    62  6   US-10-647-732A-3        Sequence 3, Appli
     3 231.5  58.9    47  6   US-10-647-732A-2        Sequence 2, Appli
     4 158.5  40.3    35  6   US-10-647-732A-1        Sequence 1, Appli
     5 118.5  30.2   105  7   US-11-228-458-10        Sequence 10, Appl
     6 118.5  30.2   105  7   US-11-228-458-14        Sequence 14, Appl
     7 118.5  30.2   130  7   US-11-043-788-222       Sequence 222, App
     8 118.5  30.2   137  7   US-11-043-788-221       Sequence 221, App
```

9	118.5	30.2	137	7	US-11-043-788-226	Sequence 226, App
10	118.5	30.2	153	7	US-11-043-788-223	Sequence 223, App
11	118.5	30.2	153	7	US-11-043-788-228	Sequence 228, App
12	118.5	30.2	153	7	US-11-244-925-4	Sequence 4, Appli
13	118.5	30.2	567	6	US-10-954-468-8	Sequence 8, Appli
14	118.5	30.2	574	6	US-10-954-468-4	Sequence 4, Appli
15	118.5	30.2	580	6	US-10-954-468-6	Sequence 6, Appli
16	118.5	30.2	587	6	US-10-954-468-2	Sequence 2, Appli
17	118.5	30.2	615	6	US-10-954-468-7	Sequence 7, Appli
18	118.5	30.2	622	6	US-10-954-468-3	Sequence 3, Appli
19	118.5	30.2	628	6	US-10-954-468-5	Sequence 5, Appli
20	118.5	30.2	633	6	US-10-954-468-1	Sequence 1, Appli
21	111.5	28.4	105	7	US-11-228-458-12	Sequence 12, Appl
22	93	23.7	195	7	US-11-043-788-220	Sequence 220, App
23	93	23.7	195	7	US-11-043-788-227	Sequence 227, App
24	83	21.1	110	7	US-11-228-458-2	Sequence 2, Appli
25	83	21.1	139	7	US-11-043-788-224	Sequence 224, App
26	83	21.1	142	7	US-11-043-788-225	Sequence 225, App
27	81	20.6	111	7	US-11-228-458-6	Sequence 6, Appli
28	78	19.8	111	7	US-11-228-458-4	Sequence 4, Appli
29	74	18.8	19	7	US-11-043-788-487	Sequence 487, App
30	66	16.8	430	7	US-11-096-568A-25863	Sequence 25863, A
31	62.5	15.9	144	7	US-11-096-568A-19656	Sequence 19656, A
32	62.5	15.9	155	7	US-11-096-568A-19655	Sequence 19655, A
33	62.5	15.9	218	7	US-11-096-568A-19654	Sequence 19654, A
34	62.5	15.9	330	7	US-11-188-298-2721	Sequence 2721, Ap
35	62.5	15.9	1158	6	US-10-501-035-366	Sequence 366, App
36	62.5	15.9	1158	7	US-11-075-646-6	Sequence 6, Appli
37	62	15.8	346	6	US-10-467-657-2676	Sequence 2676, Ap
38	62	15.8	800	7	US-11-087-099-11477	Sequence 11477, A
39	62	15.8	948	6	US-10-523-477-14	Sequence 14, Appl
40	61.5	15.6	260	7	US-11-096-568A-19639	Sequence 19639, A
41	61.5	15.6	370	7	US-11-096-568A-28786	Sequence 28786, A
42	61.5	15.6	494	7	US-11-096-568A-28785	Sequence 28785, A
43	61.5	15.6	506	7	US-11-096-568A-28784	Sequence 28784, A
44	61.5	15.6	1009	6	US-10-514-531-11	Sequence 11, Appl
45	61	15.5	643	7	US-11-137-465-54	Sequence 54, Appl

SCORE Search Results Details for Application 10647732 and Search Result us-10-647-732a-4.rpr.

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rpr.

start

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OM protein - protein search, using sw model

Run on:          April 26, 2006, 02:19:02 ; Search time 29.9669 Seconds
                                             (without alignments)
                                             237.596 Million cell updates/sec

Title:           US-10-647-732A-4
Perfect score:   393
Sequence:        1 RSVRAQRHTDMPRTPKVSTA..........KEVHQKNSSRGNTGGRNYRM 74

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:     283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

```
                              SUMMARIES
                   %
Result           Query
   No.    Score  Match  Length  DB    ID                  Description
---------------------------------------------------------------------------
     1     393   100.0    188    2    A54270              insulin-like growt
     2     393   100.0    188    2    B54270              insulin-like growt
```

3	347	88.3	155	2	C44012	insulin-like growt
4	304	77.4	176	2	A41396	insulin-like growt
5	299	76.1	176	2	A46244	insulin-like growt
6	231.5	58.9	161	2	C54270	insulin-like growt
7	207.5	52.8	79	2	I51240	insulin-like growt
8	174.5	44.4	193	2	A53697	insulin-like growt
9	158.5	40.3	149	2	D54270	insulin-like growt
10	126.5	32.2	153	2	A41399	insulin-like growt
11	118.5	30.2	137	1	IGGP1	insulin-like growt
12	118.5	30.2	137	2	A36552	insulin-like growt
13	118.5	30.2	153	1	IGHU1	insulin-like growt
14	117.5	29.9	153	2	A36079	insulin-like growt
15	114.5	29.1	153	2	S12825	insulin-like growt
16	113.5	28.9	138	2	S22878	insulin-like growt
17	113.5	28.9	153	1	IGBO1	insulin-like growt
18	113.5	28.9	154	2	JC2483	insulin-like growt
19	113.5	28.9	154	2	A33390	insulin-like growt
20	111.5	28.4	127	2	B40912	insulin-like growt
21	111.5	28.4	127	2	A25540	insulin-like growt
22	111.5	28.4	153	2	B27804	insulin-like growt
23	97.5	24.8	122	2	PN0622	insulin-like growt
24	93	23.7	195	1	IGHU1B	insulin-like growt
25	82.5	21.0	181	2	A27804	insulin-like growt
26	78	19.8	133	2	A40912	insulin-like growt
27	78	19.8	159	2	A26859	insulin-like growt
28	75.5	19.2	129	2	G36790	hypothetical prote
29	70.5	17.9	190	2	JC6062	ribosomal protein
30	69	17.6	1937	2	T03224	probable polyketid
31	68.5	17.4	212	2	C70898	hypothetical prote
32	67.5	17.2	1791	2	T02345	hypothetical prote
33	66.5	16.9	291	2	T27534	hypothetical prote
34	66	16.8	551	2	C84549	probable ubiquitin
35	66	16.8	1500	2	T03824	probable immediate
36	65.5	16.7	1148	2	T09073	splicing factor Si
37	64	16.3	234	2	T45709	hypothetical prote
38	64	16.3	263	2	S64857	hypothetical prote
39	64	16.3	535	2	C36811	hypothetical prote
40	64	16.3	535	2	A37994	RF1 protein - saim
41	63.5	16.2	310	2	S36581	E2 protein - human
42	63.5	16.2	483	2	F71619	hypothetical prote
43	63.5	16.2	2441	2	D71623	erythrocyte membra
44	63	16.0	489	2	T26069	hypothetical prote
45	63	16.0	1762	2	T03222	probable polyketid

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rup.
start

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OM protein - protein search, using sw model

Run on:           April 26, 2006, 02:14:17 ; Search time 178.579 Seconds
                                             (without alignments)
                                             292.359 Million cell updates/sec

Title:            US-10-647-732A-4
Perfect score:    393
Sequence:         1 RSVRAQRHTDMPRTPKVSTA.........KEVHQKNSSRGNTGGRNYRM 74

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        UniProt_05.80:*
                  1:  uniprot_sprot:*
                  2:  uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	188	2	Q91965_ONCTS	Q91965 oncorhynchu
2	387	98.5	188	1	IGF1_ONCKI	P17085 oncorhynchu
3	337	85.8	186	2	Q800Y5_SIGGU	Q800y5 siganus gut
4	329	83.7	186	2	O93527_PAROL	O93527 paralichthy
5	326	83.0	186	2	Q5Q0U4_DICLA	Q5q0u4 dicentrarch
6	326	83.0	186	2	Q5U8T6_EPICO	Q5u8t6 epinephelus
7	326	83.0	186	2	Q6R527_EPICO	Q6r527 epinephelus
8	326	83.0	186	2	Q70BT6_PERFL	Q70bt6 perca fluvi
9	326	83.0	186	2	Q7T1A7_PERFV	Q7t1a7 perca flave
10	326	83.0	186	2	Q9PSX5_PAROL	Q9psx5 paralichthy
11	321	81.7	186	2	Q6T8S2_MUGCE	Q6t8s2 mugil cepha
12	315	80.2	185	2	Q9YI57_ACASC	Q9yi57 acanthopagr
13	315	80.2	185	2	Q4G1F3_SPAAU	Q4g1f3 sparus aura
14	299	76.1	176	1	IGF1_ONCMY	Q02815 oncorhynchu

15	270	68.7	184	2	O42336_MYOSC	O42336	myoxocephal
16	258	65.6	182	2	O73720_OREMO	O73720	oreochromis
17	258	65.6	182	2	P79824_OREMO	P79824	oreochromis
18	251	63.9	182	2	O42289_OREMO	O42289	oreochromis
19	231.5	58.9	161	2	Q91230_ONCTS	Q91230	oncorhynchu
20	220	56.0	185	2	O57436_PAROL	O57436	paralichthy
21	213.5	54.3	161	2	Q90VV9_BRARE	Q90vv9	brachydanio
22	211.5	53.8	161	1	IGF1A_CYPCA	Q90325	cyprinus ca
23	210.5	53.6	159	2	Q6V293_ICTPU	Q6v293	ictalurus p
24	207.5	52.8	79	2	P81416_ONCKE	P81416	oncorhynchu
25	204.5	52.0	161	2	Q506L8_9TELE	Q50618	cirrhinus m
26	204	51.9	160	2	Q70BT5_PERFL	Q70bt5	perca fluvi
27	196.5	50.0	117	2	Q9I9I4_CTEID	Q9i9i4	ctenopharyn
28	196.5	50.0	161	2	Q800D5_9TELE	Q800d5	megalobrama
29	196.5	50.0	161	2	Q98SR6_MEGAM	Q98sr6	megalobrama
30	192.5	49.0	159	2	O93607_PAROL	O93607	paralichthy
31	192.5	49.0	161	2	Q9PWK2_CARAU	Q9pwk2	carassius a
32	192.5	49.0	161	2	Q9YI82_CARAU	Q9yi82	carassius a
33	192.5	49.0	178	2	Q5BQH3_9TELE	Q5bqh3	gymnocypris
34	187.5	47.7	161	1	IGF1B_CYPCA	Q90326	cyprinus ca
35	187.5	47.7	178	2	Q9IBI0_CYPCA	Q9ibi0	cyprinus ca
36	174.5	44.4	193	2	Q7LZC6_CLAMA	Q7lzc6	clarias mac
37	158.5	40.3	149	2	Q91231_ONCTS	Q91231	oncorhynchu
38	126.5	32.2	124	1	IGF1_COTJA	P51462	coturnix co
39	126.5	32.2	153	1	IGF1_CHICK	P18254	gallus gall
40	123.5	31.4	153	2	O93380_MELGA	O93380	meleagris g
41	118.5	30.2	130	1	IGF1_CAVPO	P17647	cavia porce
42	118.5	30.2	130	2	Q9NP10_HUMAN	Q9np10	homo sapien
43	118.5	30.2	137	2	Q14620_HUMAN	Q14620	homo sapien
44	118.5	30.2	153	1	IGF1A_HUMAN	P01343	homo sapien
45	118.5	30.2	153	2	Q5U743_HUMAN	Q5u743	homo sapien